## RECEIVED

MAR - 7 2002

## **TECH CENTER 1600/2900**



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/582,337

DATE: 01/25/2002 TIME: 11:56:57

Input Set : A:\Sequence.txt

```
3 <110> APPLICANT: Japan Tobacco, Inc.
      5 <120> TITLE OF INVENTION: Monoclonal Antibody Against Connective Tissue Growth Factor
              and Medicinal Uses Thereof
      8 <130> FILE REFERENCE: J1-009PCT
C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/582,337
                                                              ENTERED
C--> 11 <141> CURRENT FILING DATE: 2000-06-23
     13 <150> PRIOR APPLICATION NUMBER: JP P1997-367699
     14 <151> PRIOR FILING DATE: 1997-12-25
     16 <150> PRIOR APPLICATION NUMBER: JP P1998-356183
     17 <151> PRIOR FILING DATE: 1998-12-15
     19 <160> NUMBER OF SEQ ID NOS: 27
     21 <170> SOFTWARE: PatentIn Ver. 2.0
     23 <210> SEQ ID NO: 1
     24 <211> LENGTH: 2338
     25 <212> TYPE: DNA
     26 <213> ORGANISM: Rat
     28 <220> FEATURE:
     29 <221> NAME/KEY: 5'UTR
     30 <222> LOCATION: (1)..(212)
     32 <220> FEATURE:
     33 <221> NAME/KEY: CDS
     34 <222> LOCATION: (213)..(1256)
     36 <220> FEATURE:
     37 <221> NAME/KEY: 3'UTR
     38 <222> LOCATION: (1257)..(2338)
     40 <220> FEATURE:
     41 <221> NAME/KEY: polyA_signal
     42 <222> LOCATION: (2297)..(2302)
     44 <400> SEQUENCE: 1
     45 ctccaagaag actcagccag acccactcca gctccgaccc taggagaccg acctcctcca 60
     47 gacggcagca gccccagccc agtggacaac cccaggagcc accacctgga gcgtccggac 120
     49 accaacetee geoegagae egagteeagg eteeggeege geecetegte geetetgeae 180
     51 coogctgtgc gtootootgc ogogooooga oo atg oto goo too gto gog ggt
     52
                                            Met Leu Ala Ser Val Ala Gly
     53
     55 ccc gtt agc ctc gcc ttg gtg ctc ctc ctc tgc acc cgg cct gcc acc
     56 Pro Val Ser Leu Ala Leu Val Leu Leu Cys Thr Arg Pro Ala Thr
                 10
                                     15
     59 ggc cag gac tgc agc gcg cag tgt cag tgc gca cgt gaa gcg gcg ccg
                                                                          329
     60 Gly Gln Asp Cys Ser Ala Gln Cys Gln Cys Ala Arg Glu Ala Ala Pro
                                 30
     63 ege tge eee gee gge gtg age etg gtg etg gae gge tge tge tge
     64 Arg Cys Pro Ala Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys
```

Input Set : A:\Sequence.txt

65 40		45		50			55
67 cgc gtc tg	c gcc aag	g cag ctg	gga gaa	ctg tgc	acg gag	cgt gat	ccc 425
68 Arg Val Cy	s Ala Lys	Gln Leu	Gly Glu	Leu Cys	Thr Glu	Arg Asp	Pro
69	. 60	)		65		70	
71 tgc gac cc							
72 Cys Asp Pr	o His Lys	Gly Leu	Phe Cys	Asp Phe	Gly Ser	Pro Ala	Asn
73	75		80			85	
75 cgc aag at	t ggc gtg	tgc cct	gcc aaa	gat ggt	gca ccc	tgt gtc	ttc 521
76 Arg Lys Il	e Gly Val	Cys Pro	Ala Lys	Asp Gly	Ala Pro	Cys Val	Phe
77 9	0		95	•	100		
79 ggt ggg tc	c gtg tad	c cgc agc	ggc gag	tcc ttc	caa agc	agt tgc	aaa 569
80 Gly Gly Se	r Val Ty	Arg Ser	Gly Glu	Ser Phe	Gln Ser	Ser Cys	Lys
81 105		110			115		
83 tac cag tg	c act tgo	ctg gat	ggg gcc	gtg ggc	tgt gtg	ccc ctg	tgc 617
84 Tyr Gln Cy	s Thr Cys	Leu Asp	Gly Ala	Val Gly	Cys Val	Pro Leu	Cys
85 120		125		130			135
87 agc atg ga	c gtg cg	c ctg ccc	agc cct	gac tgc	ccc ttc	ccg aga	agg 665
88 Ser Met As							
89	140			145		150	
91 gtc aag ct	g ccc gg	g aaa tgc	tgt gag	gag tgg	gtg tgt	gat gag	ccc 713
92 Val Lys Le							
93	155		160	_	_	165	
95 aag gac cg	c aca qto	qtt qqc	cct gcc	cta gct	gcc tac	cga ctg	gaa 761
96 Lys Asp Ar							
97 17	-	-					
	U		175		180		
	~	gac cca		atg cga		tgc ctg	gtc 809
99 gac aca tt	t ggc cci		act atg		gcc aac		
	t ggc cci		act atg Thr Met		gcc aac		
99 gac aca tt 100 Asp Thr P 101 185	t ggc cct he Gly Pi	o Asp Pro	act atg Thr Met	t Met Arg	gcc aac g Ala As: 195	n Cys Leu	Val
99 gac aca tt 100 Asp Thr P	t ggc cct he Gly Pi ca gag to	o Asp Pro 190 190 agc gco	act atg Thr Met total	t Met Arg	gcc aac g Ala As 195 c tgt gg	n Cys Leu g atg ggo	val atc 857
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a	t ggc cct he Gly Pi ca gag to	o Asp Pro 190 190 agc gco	act atg Thr Met total	t Met Arg	gcc aac g Ala As 195 c tgt gg c Cys Gl	n Cys Leu g atg ggo	val atc 857
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T	t ggc cci he Gly Pi ca gag to hr Glu Ti	o Asp Pro 190 gg agc gco p Ser Ala 205	act atg Thr Met  tgt tct Cys Se	t Met Arg t aag acc r Lys Thi 210	gcc aac g Ala As 195 c tgt gg c Cys Gl	n Cys Leu g atg ggo y Met Gly	val atc 857 Ile 215
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T 105 200 107 tcc acc c	t ggc ccf he Gly P: ca gag to hr Glu T:	no Asp Pro 190 gg agc gco pp Ser Ala 205 cc aat gao	act atg Thr Met to tgt tot Cys Ser	t Met Arg t aag acc r Lys Thr 210 c ttc tgo	gcc aac g Ala As 195 c tgt gg c Cys Gl d c agg ct	n Cys Leu g atg ggo y Met Gly g gag aag	val atc 857 Ile 215 cag 905
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T 105 200	t ggc ccf he Gly Pi ca gag to hr Glu Ti gg gtt ac rg Val Ti	no Asp Pro 190 gg agc gco pp Ser Ala 205 cc aat gao	act atg Thr Met to tgt tot Cys Ser	t Met Arg t aag acc r Lys Thr 210 c ttc tgo	gcc aac g Ala As 195 c tgt gg c Cys Gl d c agg ct	n Cys Leu g atg ggo y Met Gly g gag aag	val atc 857 Ile 215 cag 905
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T 105 200 107 tcc acc c 108 Ser Thr A	t ggc ccf he Gly P: ca gag tg hr Glu T: gg gtt ac rg Val Tl	gg agc gcc p Ser Ala 205 cc aat gac ar Asn As	act atg o Thr Met o c tgt tct a Cys Sec c aat acc o Asn Thr	t aag acc r Lys Thi 210 c ttc tgo r Phe Cys 225	gcc aac g Ala As 195 c tgt gg c Cys Gl d agg ct s Arg Le	n Cys Leu g atg ggo y Met Gly g gag aag u Glu Lys 230	val atc 857 Ile 215 cag 905 Gln
99 gac aca tt 100 Asp Thr P 101	t ggc ccf he Gly P: ca gag tg hr Glu T: gg gtt ac rg Val Ti 2: tc tgc a	gg agc gcc p Ser Ala 205 cc aat gac ar Asn Asp	act atg o Thr Met o c tgt tct a Cys Sec c aat acc o Asn The	t aag acc r Lys Thr 210 c ttc tgo r Phe Cys 225 t gaa gct	gcc aac g Ala As 195 c tgt gg c Cys Gl c agg ct s Arg Le t gac ct	g atg ggc y Met Gly g gag aag u Glu Lys 230 a gag gaa	215 cag 905 cGln aac 953
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T 105 200 107 tcc acc c 108 Ser Thr A	t ggc ccf he Gly P: ca gag tg hr Glu T: gg gtt ac rg Val Ti 2: tc tgc a	gg agc gcc p Ser Ala 205 cc aat gac ar Asn Asp	act atg o Thr Met o c tgt tct a Cys Sec c aat acc o Asn The	t aag acc r Lys Thr 210 c ttc tgo r Phe Cys 225 t gaa gct s Glu Ala	gcc aac g Ala As 195 c tgt gg c Cys Gl c agg ct s Arg Le t gac ct	g atg ggc y Met Gly g gag aag u Glu Lys 230 a gag gaa	215 cag 905 cGln aac 953
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T 105 200 107 tcc acc c 108 Ser Thr A 109 111 agt cgt c 112 Ser Arg I 113	t ggc ccf he Gly P: ca gag tg hr Glu T: gg gtt ac rg Val T) 2: tc tgc ac eu Cys Mc 235	gg agc gcc p Ser Ala 205 cc aat gac ar Asn Asp 20 cg gtc agc et Val Arg	act atg of Thr Met of tgt tct a Cys Sec c aat acc of Asn Thr g ccc tgt g Pro Cys	t aag acc r Lys Thr 210 c ttc tgo r Phe Cys 225 t gaa gct s Glu Ala	gcc aac g Ala As 195 c tgt gg c Cys Gl c agg ct s Arg Le t gac ct a Asp Le	g atg ggo y Met Gly g gag aag u Glu Lys 230 a gag gaa u Glu Glu 245	atc 857 Tile 215 Tcag 905 Gin
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T 105 200 107 tcc acc c 108 Ser Thr A 109 111 agt cgt c 112 Ser Arg I	t ggc com he Gly Pr ca gag to hr Glu Tr gg gtt ac rg Val Tl tc tgc ac eu Cys Mc 235 ag ggc ac	gg agc gcc p Ser Ala 205 cc aat gac nr Asn Asp 20 cg gtc agg et Val Arc	act atg of Thr Met of tgt tct a Cys Sec c aat acc of Asn Thr g ccc tgt g Pro Cys 240 c atc cgs	t aag acc r Lys Thr 210 c ttc tgo r Phe Cys 225 t gaa gct s Glu Ala	gcc aac g Ala As 195 c tgt gg c Cys Gl c agg ct s Arg Le t gac ct a Asp Le t aaa at	g atg ggo y Met Gly g gag aag u Glu Lys 230 a gag gaa u Glu Glu 245 t gcc aag	x val x atc 857 x Ile 215 x cag 905 x Gln 953 x aac 953 x Asn 1001
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T 105 200 107 tcc acc c 108 Ser Thr A 109 111 agt cgt c 112 Ser Arg I 113 115 att aag a 116 Ile Lys I	t ggc ccf he Gly P: ca gag tg hr Glu T: gg gtt ac rg Val T! 2: tc tgc ac eu Cys Mc 235 ag ggc ac ys Gly L	gg agc gcc p Ser Ala 205 cc aat gac nr Asn Asp 20 cg gtc agg et Val Arc	act atg of Thr Men of tgt tch a Cys Sen c aat acc of Asn Thr g ccc tgh g Pro Cys c atc cgg s Ile Arg	t aag acc r Lys Thr 210 c ttc tgo r Phe Cys 225 t gaa gct s Glu Ala	gcc aac g Ala As 195 c tgt gg c Cys Gl c agg ct s Arg Le t gac ct a Asp Le t aaa at	g atg ggc y Met Gly g gag aag u Glu Lys a gag gaa u Glu Glu 245 t gcc aag e Ala Lys	x val x atc 857 x Ile 215 x cag 905 x Gln x aac 953 x Asn
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T 105 200 107 tcc acc c 108 Ser Thr A 109 111 agt cgt c 112 Ser Arg I 113 115 att aag a 116 Ile Lys I 117	t ggc ccd he Gly P: ca gag to hr Glu T: gg gtt ac rg Val Ti 2: tc tgc ac eu Cys Mc 235 ag ggc ac ys Gly Li	gg agc gcc p Ser Ala 205 cc aat gac ar Asn Asp 20 cg gtc agg ct Val Arg aa aag tgc	act atg of Thr Met of tgt tct a Cys Sec c aat acc of Asn Thr g ccc tgt g Pro Cys c atc cgc s Ile Arc 255	t aag acc r Lys Thr 210 c ttc tgo r Phe Cys 225 t gaa gct s Glu Ala	gcc aac g Ala As 195 c tgt gg c Cys Gl o agg ct s Arg Le t gac ct a Asp Le t aaa at c Lys Il 26	g atg ggc y Met Gly g gag aag u Glu Lys a gag gaa u Glu Glu 245 t gcc aag e Ala Lys	x Val x atc 857 x Ile 215 x cag 905 x Gln x aac 953 x Asn x cct 1001 x Pro
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T 105 200 107 tcc acc c 108 Ser Thr A 109 111 agt cgt c 112 Ser Arg I 113 115 att aag a 116 Ile Lys I 117 2 119 gtc aag t	t ggc ccd he Gly Pi ca gag to hr Glu Ti gg gtt ac rg Val Ti 2: tc tgc ac eu Cys Mo 235 ag ggc ac ys Gly Li 50 tt gag c	gg agc gcc p Ser Ala 205 cc aat gac r Asn Asp 20 cg gtc agc et Val Arg aa aag tgc ys Lys Cys	act atgood Thr Menor Cys Senor Cys Caat acc at acc at acc acc at acc acc at acc acc	t aag acc r Lys Thr 210 c ttc tgo r Phe Cys 225 t gaa gct s Glu Ala 0 g acg cct g Thr Pro	gcc aac J Ala As 195 c tgt gg c Cys Gl d agg ct s Arg Le t gac ct a Asp Le t aaa at Lys Il 26 J aag ac	g atg ggc g Met Gly g gag aag u Glu Lys a gag gaa u Glu Glu 245 t gcc aag e Ala Lys 0 c tac cgg	x Val 2 atc 857 7 Ile 215 7 cag 905 6 Gln 1 aac 953 1 Asn 7 cct 1001 8 Pro
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T 105 200 107 tcc acc c 108 Ser Thr A 109 111 agt cgt c 112 Ser Arg I 113 115 att aag a 116 Ile Lys I 117	t ggc ccd he Gly Pi ca gag to hr Glu Ti gg gtt ac rg Val Ti 2: tc tgc ac eu Cys Mo 235 ag ggc ac ys Gly Li 50 tt gag c	gg agc gcc p Ser Ala 205 cc aat gac r Asn Asp 20 cg gtc agc et Val Arg aa aag tgc ys Lys Cys	act atgood Thr Metology Cys This	t aag acc r Lys Thr 210 c ttc tgo r Phe Cys 225 t gaa gct s Glu Ala 0 g acg cct g Thr Pro	gcc aac J Ala As 195 c tgt gg c Cys Gl d agg ct s Arg Le t gac ct a Asp Le t aaa at Lys Il 26 J aag ac	g atg ggc g Met Gly g gag aag u Glu Lys a gag gaa u Glu Glu 245 t gcc aag e Ala Lys 0 c tac cgg	x Val 2 atc 857 7 Ile 215 7 cag 905 6 Gln 1 aac 953 1 Asn 7 cct 1001 8 Pro
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T 105 200 107 tcc acc c 108 Ser Thr A 109 111 agt cgt c 112 Ser Arg I 113 115 att aag a 116 Ile Lys I 117 2 119 gtc aag t 120 Val Lys P 121 265	t ggc ccd he Gly Pi  ca gag to hr Glu Ti  gg gtt ac rg Val Ti  2: tc tgc ac eu Cys Mo 235 ag ggc ac ys Gly Lo 50 tt gag cc he Glu Lo	gg agc gcc p Ser Ala 205 cc aat gac ar Asn Asp 20 cg gtc agg et Val Arg aa aag tgc ys Lys Cys ct tct ggc eu Ser Gl	act atgood Thr Metology Cys The	t aag acc r Lys Thr 210 c ttc tgo r Phe Cys 225 t gaa gct s Glu Ala 0 g acg cct g Thr Pro	gcc aac J Ala As 195 c tgt gg c Cys Gl o agg ct s Arg Le t gac ct a Asp Le t aaa at c Lys Il gag ac l Lys Th 275	g atg ggc y Met Gly g gag aag u Glu Lys 230 a gag gaa u Glu Glu 245 t gcc aag e Ala Lys 0 c tac cgg	x Val x atc 857 x Ile 215 x cag 905 x Gln x aac 953 x Asn x cct 1001 x Pro x gct 1049 x Ala
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T 105 200 107 tcc acc c 108 Ser Thr A 109 111 agt cgt c 112 Ser Arg I 113 115 att aag a 116 Ile Lys I 117 119 gtc aag t 120 Val Lys P 121 265 123 aag ttc t	t ggc ccf he Gly P: ca gag tg hr Glu T: gg gtt ac rg Val T! 2: tc tgc ac eu Cys Mc 235 ag ggc ac ys Gly Li 50 tt gag cc he Glu Lo	TO Asp Pro 190 gg agc gcc gp Ser Ala 205 cc aat gac ar Asn Asp 20 cg gtc agg et Val Arg aa aag tgc ys Lys Cys ct tct ggc eu Ser Gly cg tgc acg	act atgood Thr Metology Cys This	t Met Arg t aag acc r Lys Thr 210 c ttc tgo r Phe Cys 225 t gaa gct s Glu Ala 0 g acg cct g Thr Pro	gcc aac J Ala As 195 c tgt gg c Cys Gl o agg ct s Arg Le t gac ct a Asp Le t aaa at b Lys Il 26 J aag ac l Lys Th 275 c tgc ac	g atg ggc y Met Gly g gag aag u Glu Lys 230 a gag gaa u Glu Glu 245 t gcc aag e Ala Lys 0 c tac cgg r Tyr Arg	x Val
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T 105 200 107 tcc acc c 108 Ser Thr A 109 111 agt cgt c 112 Ser Arg L 113 115 att aag a 116 Ile Lys I 117 119 gtc aag t 120 Val Lys P 121 265 123 aag ttc t 124 Lys Phe C	t ggc ccf he Gly P: ca gag tg hr Glu T: gg gtt ac rg Val T! 2: tc tgc ac eu Cys Mc 235 ag ggc ac ys Gly Li 50 tt gag cc he Glu Lo	TO Asp Pro 190 gg agc gcc gp Ser Ala 205 cc aat gac ar Asn Asp 20 cg gtc agg et Val Arg aa aag tgc ys Lys Cys ct tct ggc eu Ser Gly cg tgc acg	act atgood Thr Metology Cys This	t Met Arg t aag acc r Lys Thr 210 c ttc tgo r Phe Cys 225 t gaa gct s Glu Ala 0 g acg cct g Thr Pro	gcc aac y Ala As 195 c tgt gg c Cys Gl c agg ct s Arg Le t gac ct a Asp Le t aaa at b Lys Il 26 g aag ac l Lys Th 275 c tgc ac s Cys Th	g atg ggc y Met Gly g gag aag u Glu Lys 230 a gag gaa u Glu Glu 245 t gcc aag e Ala Lys 0 c tac cgg r Tyr Arg	x Val
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T 105 200 107 tcc acc c 108 Ser Thr A 109 111 agt cgt c 112 Ser Arg L 113 115 att aag a 116 Ile Lys I 117 119 gtc aag t 120 Val Lys P 121 265 123 aag ttc t 124 Lys Phe C 125 280	t ggc ccd he Gly Pi  ca gag tg hr Glu Ti  gg gtt ac rg Val Ti  22 tc tgc ac eu Cys Mc 235 ag ggc ac ys Gly Li 50 he Glu Lo gt ggg g	ro Asp Pro 190 gg agc gcc rp Ser Ala 205 cc aat gac ar Asn Asp 20 gg gtc agg et Val Arg aa aag tgc ys Lys Cys ct tct ggc tg tgc acc al Cys Thi 285	act atgood Thr Metology Cys Services at according Pro Cys 240 at according Cys The Cys	t Met Arg t aag acc r Lys Thr 210 c ttc tgc r Phe Cys 225 t gaa gct s Glu Ala 0 g acg cct g Thr Pro c agt gtg r Ser Val c cgc tgc y Arg Cys 290	gcc aac y Ala As 195 c tgt gg c Cys Gl c agg ct s Arg Le t gac ct a Asp Le t aaa at b Lys Il 26 g aag ac l Lys Th 275 c tgc ac s Cys Th	g atg ggo y Met Gly g gag aag u Glu Lys 230 a gag gaa u Glu Glu 245 t gcc aag e Ala Lys 0 c tac cgg r Tyr Arg	atc 857 Tile 215 T cag 905 T cag 905 T aac 953 T Asn T cct 1001 T pro T gct 1049 T Ala T aga 1097 T Arg 295
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T 105 200 107 tcc acc c 108 Ser Thr A 109 111 agt cgt c 112 Ser Arg L 113 115 att aag a 116 Ile Lys I 117 119 gtc aag t 120 Val Lys P 121 265 123 aag ttc t 124 Lys Phe C 125 280 127 acc acc a	t ggc ccd he Gly Pi  ca gag to hr Glu Ti  gg gtt ac rg Val Ti  tc tgc a eu Cys Mc 235 ag ggc ac ys Gly Li 50 tt gag c he Glu Lo gt ggg g ys Gly V ca ctg c	TO Asp Pro 190 gg agc gcc gp Ser Ala 205 cc aat gac ar Asn Asp 20 gg gtc agg et Val Arg aa aag tgc ys Lys Cys ct tct ggc ac cg tg tgc acc al Cys Th: 285 cg gtg gag	act atg of Thr Men of tgt tch a Cys Sen c aat acc of Asn Thr g ccc tgh g Pro Cys 240 c atc cgg s Ile Arg 255 c tgc acc y Cys Thi of gac ggo r Asp Gl g ttc aag	t Met Arg t aag acc r Lys Thr 210 c ttc tgc r Phe Cys 225 t gaa gct s Glu Ala 0 g acg cct g Thr Pro c agt gtg r Ser Val c cgc tgc y Arg Cys 290 g tgc ccc	gcc aac J Ala As 195 c tgt gg c Cys Gl c agg ct s Arg Le t gac ct a Asp Le t aaa at b Lys Il 26 J aag ac l Lys Th 275 c tgc ac c Cys Th c gat gg	g atg ggo y Met Gly g gag aag u Glu Lys 230 a gag gaa u Glu Glu 245 t gcc aag e Ala Lys 0 c tac cgg r Tyr Arg a ccg cac r Pro His	x Val x atc 857 x Ile 215 x cag 905 x Gln 905 x aac 953 x Asn 1001 x pro 1049 x Arg 295 x atg 1145
99 gac aca tt 100 Asp Thr P 101 185 103 cag acc a 104 Gln Thr T 105 200 107 tcc acc c 108 Ser Thr A 109 111 agt cgt c 112 Ser Arg L 113 115 att aag a 116 Ile Lys I 117 119 gtc aag t 120 Val Lys P 121 265 123 aag ttc t 124 Lys Phe C 125 280	t ggc cci he Gly Pi ca gag to hr Glu Ti gg gtt ac rg Val Ti 2: tc tgc ac eu Cys Mc 235 ag ggc ac ys Gly Li 50 tt gag cci he Glu Lo gt ggg g ys Gly Vo ca ctg cci hr Leu Pi	TO Asp Pro 190 gg agc gcc gp Ser Ala 205 cc aat gac ar Asn Asp 20 gg gtc agg et Val Arg aa aag tgc ys Lys Cys ct tct ggc ac cg tg tgc acc al Cys Th: 285 cg gtg gag	act atg of Thr Men of tgt tch a Cys Sen c aat acc of Asn Thr g ccc tgh g Pro Cys 240 c atc cgg s Ile Arg 255 c tgc acc y Cys Thi of gac ggo r Asp Gl g ttc aag	t Met Arg t aag acc r Lys Thr 210 c ttc tgc r Phe Cys 225 t gaa gct s Glu Ala 0 g acg cct g Thr Pro c agt gtg r Ser Val c cgc tgc y Arg Cys 290 g tgc ccc	gcc aac J Ala As 195 c tgt gg c Cys Gl c agg ct s Arg Le t gac ct a Asp Le t aaa at b Lys Il 26 J aag ac l Lys Th 275 c tgc ac c Cys Th c gat gg	g atg ggo y Met Gly g gag aag u Glu Lys 230 a gag gaa u Glu Glu 245 t gcc aag e Ala Lys 0 c tac cgg r Tyr Arg a ccg cac r Pro His	x Val x atc 857 x Ile 215 x cag 905 x Gln 905 x aac 953 x Asn 1001 x pro 1049 x Ala 1097 x Arg 295 x atg 1145 x Met

Input Set : A:\Sequence.txt

	aaa aag Lys Lys															1193
	ccc ggg			<b>426</b>	a+c	+++	asa		tta	tac	tac	aaa		atα	tat	1241
	Pro Gly															1241
137	110 017	330		пор	110	1.1.0	335			-1-	-1-	340			-1-	
	gga gac		aca	taa	agco	caqqq	gag 1	aago	qaca	ac qa	aacto	catti	t aga	actat	taac	1296
	Gly Asp	-			•	,,,	, ,		, ,	_			-			
141	345	ı														
143	ttgaact	gag	ttaca	atcto	ca ti	tttct	ttct	, taa	aaaa	aaac	aaaa	aaggg	gtt a	acagt	tagcac	1356
	attaatt															
	cgtgtgt															
	gacttga															
	aagagtg															
	atgccta															
	gctctag															
	cagtaag		_	-	_	-										
	gaacctt															
	tttttat															
	aatttaa															
	atagcct															
	aggagat agacggt															
	gcgaaca															
	aggaagt															
																2230
	atataac	Caa :	aanti	racat	ra ti	ttaca	acct1	- tai	tagti	taaa	aata	aaagi	tat :	atata	attttt	2316
			-		_	-	accti	tc1	tagti	tgaa	aata	aaagt	tat a	atata	attttt	
177	tatatga	aaa	aaaaa	aaaa	_	-	accti	t to	tagti	tgaa	aata	aaagt	tat a	atata	attttt	2316 2338
177 180	tatatga <210> S	aaa a EQ II	aaaaa D NO	aaaa : 2	_	-	accti	tc1	tagti	tgaa	aata	aaagt	tat (	atata	attttt	
177 180 181	tatatga <210> S <211> I	aaa a EQ II ENGT	aaaaa D NO H: 34	aaaa : 2	_	-	accti	tei	tagti	tgaa	aata	aaag1	tat i	atata	atttt	
177 180 181 182	tatatga <210> S <211> I <212> T	aaa a EQ II ENGTI	aaaaa D NO H: 34 PRT	aaaa : 2 47	_	-	accti	te1	tagti	tgaa	aata	aaag1	tat i	atata	atttt	
177 180 181 182 183	tatatga <210> S <211> I	aaa a EQ II ENGTI YPE:	aaaaa D NO H: 34 PRT ISM:	aaaaa : 2 47 Rat	_	-	acct1	tc1	tagt1	tgaa	aata	aaagt	tat :	atata	atttt	
177 180 181 182 183 185	tatatga <210> S <211> I <212> T <213> C	aaa a EQ II ENGTI YPE: RGANI	aaaaa D NO H: 34 PRT ISM: NCE:	aaaaa : 2 47 Rat 2	aa aa	a										
177 180 181 182 183 185	tatatga <210> S <211> I <212> T <213> C <400> S	aaa a EQ II ENGTI YPE: RGANI	aaaaa D NO H: 34 PRT ISM: NCE:	aaaaa : 2 47 Rat 2	aa aa	a										
177 180 181 182 183 185 186	tatatga <210> S <211> I <212> T <213> C <400> S Met Leu	aaa a EQ II ENGT YPE: RGAN EQUE Ala	aaaaa D NO H: 34 PRT ISM: NCE: Ser	aaaaa : 2 47 Rat 2 Val	aa aa	Gly	Pro	Val	Ser 10	Leu	Ala	Leu	Val	Leu 15	Leu	
177 180 181 182 183 185 186 187 189	tatatga <210> S <211> I <212> T <213> C <400> S Met Leu 1 Leu Cys	aaa a EQ II ENGT YPE: RGAN EQUE Ala	aaaaa D NO H: 34 PRT ISM: NCE: Ser Arg 20	Rat 2 Val 5 Pro	Ala	Gly	Pro Gly	Val Gln 25	Ser 10 Asp	Leu Cys	Ala Ser	Leu Ala	Val Gln 30	Leu 15 Cys	Leu Gln	
177 180 181 182 183 185 186 187 189	tatatga <210> S <211> I <212> T <213> C <400> S Met Leu 1	aaa a EQ II ENGT YPE: RGAN EQUE Ala	aaaaa D NO H: 34 PRT ISM: NCE: Ser Arg 20	Rat 2 Val 5 Pro	Ala	Gly	Pro Gly	Val Gln 25	Ser 10 Asp	Leu Cys	Ala Ser	Leu Ala	Val Gln 30	Leu 15 Cys	Leu Gln	
177 180 181 182 183 185 186 187 189 190 192 193	tatatga <210> S <211> I <212> T <213> C <400> S Met Leu 1 Leu Cys	aaa aEQ II ENGTI YPE: RGAN EQUE Ala Thr	aaaaa D NO H: 34 PRT ISM: NCE: Ser Arg 20 Glu	Rat 2 Val 5 Pro	Ala Ala Ala	Gly Thr	Pro Gly Arg 40	Val Gln 25 Cys	Ser 10 Asp	Leu Cys Ala	Ala Ser Gly	Leu Ala Val 45	Val Gln 30 Ser	Leu 15 Cys Leu	Leu Gln Val	
177 180 181 182 183 185 186 187 189 190 192 193	tatatga <210> S <211> I <212> T <213> C <400> S Met Leu 1 Leu Cys	aaa aEQ II ENGTI YPE: RGAN EQUE Ala Thr	aaaaa D NO H: 34 PRT ISM: NCE: Ser Arg 20 Glu	Rat 2 Val 5 Pro	Ala Ala Ala	Gly Thr Pro Cys	Pro Gly Arg 40 Arg	Val Gln 25 Cys Val	Ser 10 Asp Pro	Leu Cys Ala Ala	Ala Ser Gly Lys	Leu Ala Val 45 Gln	Val Gln 30 Ser	Leu 15 Cys Leu	Leu Gln Val	
177 180 181 182 183 185 186 187 189 190 192 193 195	tatatga <210> S <211> I <212> T <213> C <400> S Met Leu 1 Leu Cys Cys Ala Leu Asp	aaa a EQ II ENGT YPE: RGAN EQUE Ala Thr Arg 35 Gly	aaaaa D NO H: 34 PRT ISM: NCE: Ser Arg 20 Glu	Rat 2 Val 5 Pro Ala	Ala Ala Ala Cys	Gly Thr Pro Cys 55	Pro Gly Arg 40 Arg	Val Gln 25 Cys Val	Ser 10 Asp Pro	Leu Cys Ala Ala	Ala Ser Gly Lys	Leu Ala Val 45 Gln	Val Gln 30 Ser Leu	Leu 15 Cys Leu Gly	Leu Gln Val Glu	
177 180 181 182 183 185 186 187 199 192 193 195 196 198	tatatga <210> S <211> I <212> T <213> C <400> S Met Leu 1 Leu Cys Cys Ala Leu Asp 50 Leu Cys	aaa a EQ II ENGT YPE: RGAN EQUE Ala Thr Arg 35 Gly	aaaaa D NO H: 34 PRT ISM: NCE: Ser Arg 20 Glu	Rat 2 Val 5 Pro Ala	Ala Ala Ala Cys	Gly Thr Pro Cys 55	Pro Gly Arg 40 Arg	Val Gln 25 Cys Val	Ser 10 Asp Pro	Leu Cys Ala Ala His	Ala Ser Gly Lys	Leu Ala Val 45 Gln	Val Gln 30 Ser Leu	Leu 15 Cys Leu Gly	Leu Gln Val Glu Cys	
177 180 181 182 183 185 186 187 199 192 193 195 196 198	tatatga <210> S <211> I <212> T <213> C <400> S Met Leu 1 Leu Cys Cys Ala Leu Asp 50 Leu Cys 65	aaa a EQ II ENGT YPE: RGAN EQUE Ala Thr Arg 35 Gly	aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	Rat 2 Val 5 Pro Ala Gly	Ala Ala Ala Cys Asp	Gly Thr Pro Cys 55 Pro	Pro Gly Arg 40 Arg Cys	Val Gln 25 Cys Val Asp	Ser 10 Asp Pro Cys	Leu Cys Ala Ala His	Ala Ser Gly Lys 60 Lys	Leu Ala Val 45 Gln Gly	Val Gln 30 Ser Leu Leu	Leu 15 Cys Leu Gly	Leu Gln Val Glu Cys 80	
177 180 181 182 183 185 186 187 189 190 192 193 195 196 198 199 201	tatatga <210> S <211> I <212> T <213> C <400> S Met Leu 1 Leu Cys Cys Ala Leu Asp 50 Leu Cys	aaa a EQ II ENGT YPE: RGAN EQUE Ala Thr Arg 35 Gly	aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	Rat 2 Val 5 Pro Ala Gly Arg	Ala Ala Ala Cys Asp	Gly Thr Pro Cys 55 Pro	Pro Gly Arg 40 Arg Cys	Val Gln 25 Cys Val Asp	Ser 10 Asp Pro Cys Pro Ile	Leu Cys Ala Ala His	Ala Ser Gly Lys 60 Lys	Leu Ala Val 45 Gln Gly	Val Gln 30 Ser Leu Leu	Leu 15 Cys Leu Gly Phe	Leu Gln Val Glu Cys 80	
177 180 181 182 183 185 186 187 189 190 192 193 195 196 198 199 201 202	tatatga <210> S <211> I <212> T <213> C <400> S Met Leu Leu Cys Cys Ala Leu Asp 50 Leu Cys 65 Asp Phe	aaa a a a a a a a a a a a a a a a a a	aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	Rat 2 Val 5 Pro Ala Gly Arg	Ala Ala Ala Cys Asp 70 Ala	Gly Thr Pro Cys 55 Pro Asn	Pro Gly Arg 40 Arg Cys	Val Cln 25 Cys Val Asp Lys	Ser 10 Asp Pro Cys Pro Ile 90	Leu Cys Ala Ala His 75 Gly	Ala Ser Gly Lys 60 Lys Val	Leu Ala Val 45 Gln Gly Cys	Val Gln 30 Ser Leu Leu Pro	Leu 15 Cys Leu Gly Phe Ala 95	Leu Gln Val Glu Cys 80 Lys	
177 180 181 182 183 185 186 187 189 190 192 193 195 196 198 199 201 202 204	tatatga <210> S <211> I <212> T <213> C <400> S Met Leu 1 Leu Cys Cys Ala Leu Asp 50 Leu Cys 65 Asp Phe	aaa a a a a a a a a a a a a a a a a a	aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	Rat 2 Val 5 Pro Ala Gly Arg	Ala Ala Ala Cys Asp 70 Ala	Gly Thr Pro Cys 55 Pro Asn	Pro Gly Arg 40 Arg Cys	Val Gln 25 Cys Val Asp Lys Gly	Ser 10 Asp Pro Cys Pro Ile 90	Leu Cys Ala Ala His 75 Gly	Ala Ser Gly Lys 60 Lys Val	Leu Ala Val 45 Gln Gly Cys	Val Gln 30 Ser Leu Leu Pro Ser	Leu 15 Cys Leu Gly Phe Ala 95	Leu Gln Val Glu Cys 80 Lys	
177 180 181 182 183 185 186 187 189 190 192 193 195 196 198 199 201 202 204 205	tatatga <210> S <211> I <212> T <213> C <400> S Met Leu 1 Leu Cys Cys Ala Leu Asp 50 Leu Cys 65 Asp Phe	aaa a a a a a a a a a a a a a a a a a	aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	Rat 2 Val 5 Pro Ala Gly Pro 85 Cys	Ala Ala Ala Cys Asp 70 Ala	Gly Thr Pro Cys 55 Pro Asn Phe	Pro Gly Arg 40 Arg Cys Arg	Val Gln 25 Cys Val Asp Lys Gly 105	Ser 10 Asp Pro Cys Pro Ile 90 Ser	Leu Cys Ala Ala His 75 Gly Val	Ala Ser Gly Lys 60 Lys Val	Leu Ala Val 45 Gln Gly Cys	Val Gln 30 Ser Leu Pro Ser 110	Leu 15 Cys Leu Gly Phe Ala 95 Gly	Leu Gln Val Glu Cys 80 Lys Glu	
177 180 181 182 183 185 186 187 189 190 192 193 195 196 198 199 201 202 204 205 207	tatatga <210> S <211> I <212> T <213> C <400> S Met Leu 1 Leu Cys Cys Ala Leu Asp 50 Leu Cys 65 Asp Phe	aaa a EQ II ENGT YPE: RGAN EQUE Ala Thr Arg 35 Gly Thr Gly Ala Gln	aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	Rat 2 Val 5 Pro Ala Gly Pro 85 Cys	Ala Ala Ala Cys Asp 70 Ala	Gly Thr Pro Cys 55 Pro Asn Phe	Pro Gly Arg 40 Arg Cys Arg Gly Tyr	Val Gln 25 Cys Val Asp Lys Gly 105	Ser 10 Asp Pro Cys Pro Ile 90 Ser	Leu Cys Ala Ala His 75 Gly Val	Ala Ser Gly Lys 60 Lys Val	Leu Ala Val 45 Gln Gly Cys Arg Leu	Val Gln 30 Ser Leu Pro Ser 110	Leu 15 Cys Leu Gly Phe Ala 95 Gly	Leu Gln Val Glu Cys 80 Lys Glu	
177 180 181 182 183 185 186 187 189 190 192 193 195 196 198 199 201 202 204 205 207 208	tatatga <210> S <211> I <212> T <213> C <400> S Met Leu 1 Leu Cys Cys Ala Leu Asp 50 Leu Cys 65 Asp Phe	aaa a a a a a a a a a a a a a a a a a	aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	Rat 2 Val 5 Pro Ala Gly Arg Pro 85 Cys	Ala Ala Cys Asp 70 Ala Val	Gly Thr Pro Cys 55 Pro Asn Phe Lys	Pro Gly Arg 40 Arg Cys Arg Gly Tyr	Val Gln 25 Cys Val Asp Lys Gly 105 Gln	Ser 10 Asp Pro Cys Pro Ile 90 Ser Cys	Leu Cys Ala Ala His 75 Gly Val	Ala Ser Gly Lys 60 Lys Val Tyr Cys	Leu Ala Val 45 Gln Gly Cys Arg Leu 125	Val Gln 30 Ser Leu Pro Ser 110 Asp	Leu 15 Cys Leu Gly Phe Ala 95 Gly	Leu Gln Val Glu Cys 80 Lys Glu Ala	

Input Set : A:\Sequence.txt

```
135
211
       130
213 Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys Cys Glu
                     150
                                            155
216 Glu Trp Val Cys Asp Glu Pro Lys Asp Arg Thr Val Val Gly Pro Ala
                                        170
217
                    165
219 Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro Thr Met
                                    185
222 Met Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala Cys Ser
223
           195
                                200
225 Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp Asn Thr
                            215
                                                220
228 Phe Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg Pro Cys
                        230
                                            235
231 Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys Ile Arg
                    245
                                        250
234 Thr Pro Lys Ile Ala Lys Pro Val Lys Phe Glu Leu Ser Gly Cys Thr
235
                260
                                    265
237 Ser Val Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr Asp Gly
           275
                                280
                                                    285 .
240 Arg Cys Cys Thr Pro His Arg Thr Thr Leu Pro Val Glu Phe Lys
                            295
243 Cys Pro Asp Gly Glu Ile Met Lys Lys Asn Met Met Phe Ile Lys Thr
                                            315
246 Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe Glu Ser
247
                    325
                                        330
249 Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
250
                340
253 <210> SEQ ID NO: 3
254 <211> LENGTH: 20
255 <212> TYPE: DNA
256 <213> ORGANISM: Artificial Sequence
258 <220> FEATURE:
259 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificially
         synthesized primer sequence
262 <220> FEATURE:
263 <221> NAME/KEY: primer_bind
264 <222> LOCATION: (1)..(20)
266 <400> SEQUENCE: 3
267 tgcggctgct gccgcgtctg
                                                                       20
270 <210> SEQ ID NO: 4
271 <211> LENGTH: 21
272 <212> TYPE: DNA
273 <213> ORGANISM: Artificial Sequence
275 <220> FEATURE:
276 <223> OTHER INFORMATION: Description of Artificial Sequence: Artificially
         synthesized primer sequence
279 <220> FEATURE:
280 <221> NAME/KEY: primer_bind
281 <222> LOCATION: (1)..(21)
```

Input Set : A:\Sequence.txt

```
283 <400> SEQUENCE: 4
                                                                       21
284 gcacaggtct tgatgaacat c
287 <210> SEQ ID NO: 5
288 <211> LENGTH: 444
289 <212> TYPE: DNA
290 <213> ORGANISM: Homo sapiens
292 <220> FEATURE:
293 <221> NAME/KEY: CDS
294 <222> LOCATION: (1)..(444)
296 <220> FEATURE:
297 <221> NAME/KEY: sig_peptide
298 <222> LOCATION: (1)..(57)
300 <220> FEATURE:
301 <221> NAME/KEY: V_region
302 <222> LOCATION: (58)..(363)
304 <400> SEQUENCE: 5
305 atg gag ttt ggg ctg agc tgg att ttc ctt gct gct att tta aaa ggt
                                                                       48
306 Met Glu Phe Gly Leu Ser Trp Ile Phe Leu Ala Ala Ile Leu Lys Gly
307
                                                                       96
309 gtc cag tgt gag gtg cag ctg gtg gag tct ggg gga ggc ttg gta aag
310 Val Gln Cys Glu Val Gln Leu Val Glu Ser Gly Gly Leu Val Lys
                                     25
313 cct ggg ggg tcc ctt aag acc tct cct gtg cag cct ctg gat tca act
                                                                       144
314 Pro Gly Gly Ser Leu Lys Thr Ser Pro Val Gln Pro Leu Asp Ser Thr
315
             35
317 ttc agt aac gcc tgg atg agc tgg gtc cgc cag gct cca gga agg ggc
                                                                       192
318 Phe Ser Asn Ala Trp Met Ser Trp Val Arg Gln Ala Pro Gly Arg Gly
                             55
321 tgg agt ggg ttg gcc gta tta aaa gca aaa ctg atg gtg gga cac aca
                                                                       240
322 Trp Ser Gly Leu Ala Val Leu Lys Ala Lys Leu Met Val Gly His Thr
                         70
                                             75
323 65
325 gac tac gct gca ccc gtg aaa ggc aga ttc acc atc tca aga gat gat
                                                                       288
326 Asp Tyr Ala Ala Pro Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asp
327
                     85
329 tca aaa aac acg ctg tat ctg caa atg aac agc ctg aaa acc gag gac
                                                                       336
330 Ser Lys Asn Thr Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp
                100
                                    105
333 aca gcc gtg tat tac tgt acc aca aaa tgg gtg gct acg gac tac ttt
                                                                       384
334 Thr Ala Val Tyr Tyr Cys Thr Thr Lys Trp Val Ala Thr Asp Tyr Phe
            115
335
                                120
337 gac tac tgg ggc cag gga acc ctg gtc acc gtc tcc tca gcc tcc acc
                                                                       432
338 Asp Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr
       130
                            135
                                                140
341 aag ggc cca tcg
                                                                       444
342 Lys Gly Pro Ser
343 145
346 <210> SEQ ID NO: 6
347 <211> LENGTH: 148
348 <212> TYPE: PRT
```

VERIFICATION SUMMARY PATENT APPLICATION: US/09/582,337 DATE: 01/25/2002

TIME: 11:56:58

Input Set : A:\Sequence.txt

Output Set: N:\CRF3\01252002\I582337.raw

L:10~M:270~C: Current Application Number differs, Replaced Application Number L:11~M:271~C: Current Filing Date differs, Replaced Current Filing Date